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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Tue Oct 30 17:50:12 EDT 2007

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Application No: 10520655 Version No: 2.0

Input Set:

Output Set:

**Started:** 2007-10-09 12:57:55.239  
**Finished:** 2007-10-09 12:58:00.579  
**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 340 ms  
**Total Warnings:** 17  
**Total Errors:** 30  
**No. of SeqIDs Defined:** 18  
**Actual SeqID Count:** 18

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)

**Input Set:**

**Output Set:**

**Started:** 2007-10-09 12:57:55.239  
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**Total Warnings:** 17  
**Total Errors:** 30  
**No. of SeqIDs Defined:** 18  
**Actual SeqID Count:** 18

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (12)
E 257	Invalid sequence data feature in <221> in SEQ ID (12)
E 257	Invalid sequence data feature in <221> in SEQ ID (12)
E 257	Invalid sequence data feature in <221> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
E 257	Invalid sequence data feature in <221> in SEQ ID (14)
E 257	Invalid sequence data feature in <221> in SEQ ID (14)
E 257	Invalid sequence data feature in <221> in SEQ ID (14) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)

# SEQUENCE LISTING

<110> DIDEBERG, OTTO  
VERNET, THIERRY  
MOUZ, NICOLAS

<120> STREPTOCOCCUS PNEUMONIAE PBP2X MINI-PROTEIN AND USES  
THEREOF

<130> 70457-19

<140> 10520655

<141> 2005-03-07

<150> PCT/IB03/003397

<151> 2003-07-11

<150> FR 02/08724

<151> 2002-07-11

<160> 18

<170> PatentIn Ver. 3.3

<210> 1

<211> 551

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
mini-PBP2x construct

<400> 1

Gly Ser Gly Ala Lys Arg Gly Thr Ile Tyr Asp Arg Asn Gly Val Pro  
1 5 10 15

Ile Ala Glu Asp Ala Thr Ser Gly Gly Pro Asn Arg Ser Tyr Pro Asn  
20 25 30

Gly Gln Phe Ala Ser Ser Phe Ile Gly Gly Gly Met Glu Ser Ser Leu  
35 40 45

Asn Ser Ile Leu Ala Gly Gly Gly Gly Asp Gly Lys Asp Val Tyr Thr  
50 55 60

Thr Ile Ser Ser Pro Leu Gln Ser Phe Met Glu Thr Gln Met Asp Ala  
65 70 75 80

Phe Gln Glu Lys Val Lys Gly Lys Tyr Met Thr Ala Thr Leu Val Ser  
85 90 95

Ala Lys Thr Gly Glu Ile Leu Ala Thr Thr Gln Arg Pro Thr Phe Asp  
100 105 110

Ala Asp Thr Lys Glu Gly Ile Thr Glu Asp Phe Val Trp Arg Asp Ile

115							120						125				
Leu	Tyr	Gln	Ser	Asn	Tyr	Glu	Pro	Gly	Ser	Thr	Met	Lys	Val	Met	Met		
130						135					140						
Leu	Ala	Ala	Ala	Ile	Asp	Asn	Asn	Thr	Phe	Pro	Gly	Gly	Glu	Val	Phe		
145					150				155						160		
Asn	Ser	Ser	Glu	Leu	Lys	Ile	Ala	Asp	Ala	Thr	Ile	Arg	Asp	Trp	Asp		
				165					170					175			
Val	Asn	Glu	Gly	Leu	Thr	Gly	Gly	Arg	Met	Met	Thr	Phe	Ser	Gln	Gly		
			180					185					190				
Phe	Ala	His	Ser	Ser	Asn	Val	Gly	Met	Thr	Leu	Leu	Glu	Gln	Lys	Met		
	195						200					205					
Gly	Asp	Ala	Thr	Trp	Leu	Asp	Tyr	Leu	Asn	Arg	Phe	Lys	Phe	Gly	Val		
210						215					220						
Pro	Thr	Arg	Phe	Gly	Leu	Thr	Asp	Glu	Tyr	Ala	Gly	Gln	Leu	Pro	Ala		
225					230					235					240		
Asp	Asn	Ile	Val	Asn	Ile	Ala	Gln	Ser	Ser	Phe	Gly	Gln	Gly	Ile	Ser		
				245					250					255			
Val	Thr	Gln	Thr	Gln	Met	Ile	Arg	Ala	Phe	Thr	Ala	Ile	Ala	Asn	Asp		
		260						265					270				
Gly	Val	Met	Leu	Glu	Pro	Lys	Phe	Ile	Ser	Ala	Ile	Tyr	Asp	Pro	Asn		
	275						280					285					
Asp	Gln	Thr	Ala	Arg	Lys	Ser	Gln	Lys	Glu	Ile	Val	Gly	Asn	Pro	Val		
290						295					300						
Ser	Lys	Asp	Ala	Ala	Ser	Leu	Thr	Arg	Thr	Asn	Met	Val	Leu	Val	Gly		
305					310					315					320		
Thr	Asp	Pro	Val	Tyr	Gly	Thr	Met	Tyr	Asn	His	Ser	Thr	Gly	Lys	Pro		
				325					330					335			
Thr	Val	Thr	Val	Pro	Gly	Gln	Asn	Val	Ala	Leu	Lys	Ser	Gly	Thr	Ala		
		340						345					350				
Gln	Ile	Ala	Asp	Glu	Lys	Asn	Gly	Gly	Tyr	Leu	Val	Gly	Leu	Thr	Asp		
	355						360					365					
Tyr	Ile	Phe	Ser	Ala	Val	Ser	Met	Ser	Pro	Ala	Glu	Asn	Pro	Asp	Phe		
370						375					380						
Ile	Leu	Tyr	Val	Thr	Val	Gln	Gln	Pro	Glu	His	Tyr	Ser	Gly	Ile	Gln		
385					390					395					400		
Leu	Gly	Glu	Phe	Ala	Asn	Pro	Ile	Leu	Glu	Arg	Ala	Ser	Ala	Met	Lys		
				405					410					415			
Asp	Ser	Leu	Asn	Leu	Gln	Thr	Thr	Ala	Lys	Ala	Leu	Glu	Gln	Val	Ser		

420	425	430
Gln Gln Ser Pro Tyr Pro Met Pro Ser Val Lys Asp Ile Ser Pro Gly		
435	440	445
Asp Leu Ala Glu Glu Leu Arg Arg Asn Leu Val Gln Pro Ile Val Val		
450	455	460
Gly Thr Gly Thr Lys Ile Lys Asn Ser Ser Ala Glu Glu Gly Lys Asn		
465	470	475 480
Leu Ala Pro Asn Gln Gln Val Leu Ile Leu Ser Asp Lys Ala Glu Glu		
485	490	495
Val Pro Asp Met Tyr Gly Trp Thr Lys Glu Thr Ala Glu Thr Leu Ala		
500	505	510
Lys Trp Leu Asn Ile Glu Leu Glu Phe Gln Gly Ser Gly Ser Thr Val		
515	520	525
Gln Lys Gln Asp Val Arg Ala Asn Thr Ala Ile Lys Asp Ile Lys Lys		
530	535	540
Ile Thr Leu Thr Leu Gly Asp		
545	550	

<210> 2  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 2  
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<210> 3  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 3  
 ggatccggga caggcactcg c 21

<210> 4  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 4  
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<210> 5  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 5  
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<210> 6  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 6  
gttcaaggaa ctctccattc caccgccgat aaaactagaa gcaaattg 48

<210> 7  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 7  
tgtataaaca tccttaccgt cccacctcc cctgcaaga atactgttc 49

<210> 8  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 8  
ccgcatatgg ccaaactgtg gactatttat 30

<210> 9  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 9  
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<210> 10  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
peptide

<220>  
<221> MOD\_RES  
<222> (3)  
<223> variable amino acid

<220>  
<221> MOD\_RES  
<222> (4)  
<223> hydrophobic amino acid

<220>  
<221> MOD\_RES  
<222> (5)  
<223> variable amino acid

<220>  
<221> MOD\_RES  
<222> (6)  
<223> Asp or Ser

<220>  
<221> MOD\_RES  
<222> (10)..(12)  
<223> variable amino acid

<400> 10  
Arg Gly Xaa Xaa Xaa Xaa Arg Ser Gly Xaa Xaa Xaa Ala  
1 5 10

<210> 11



<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<220>  
<221> MOD\_RES  
<222> (1)  
<223> Arg or Lys

<220>  
<221> MOD\_RES  
<222> (2)..(3)  
<223> variable amino acid

<220>  
<221> MOD\_RES  
<222> (5)  
<223> variable amino acid

<400> 11  
Xaa Xaa Xaa Pro Xaa Gly  
1 5

<210> 12  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<220>  
<221> MOD\_RES  
<222> (1)  
<223> Gly or Tyr

<220>  
<221> MOD\_RES  
<222> (2)  
<223> hydrophobic amino acid

<220>  
<221> MOD\_RES  
<222> (4)..(6)  
<223> variable amino acid

<220>  
<221> MOD\_RES  
<222> (8)..(9)  
<223> variable amino acid

<400> 12

Xaa Xaa Glu Xaa Xaa Xaa Asp Xaa Xaa Leu

1 5 10

<210> 13

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD\_RES

<222> (1)

<223> hydrophobic amino acid

<220>

<221> MOD\_RES

<222> (2)..(3)

<223> variable amino acid

<220>

<221> MOD\_RES

<222> (4)

<223> Ser or Thr

<220>

<221> MOD\_RES

<222> (5)

<223> hydrophobic amino acid

<220>

<221> MOD\_RES

<222> (7)..(9)

<223> variable amino acid

<400> 13

Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Gln

1 5 10

<210> 14

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD\_RES

<222> (2)

<223> Gly or Ser

<220>  
<221> MOD\_RES  
<222> (4)..(5)  
<223> hydrophobic amino acid

<220>  
<221> MOD\_RES  
<222> (6)..(9)  
<223> variable amino acid

<220>  
<221> MOD\_RES  
<222> (12)  
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<220>  
<221> MOD\_RES  
<222> (13)  
<223> hydrophobic amino acid

<220>  
<221> MOD\_RES  
<222> (14)  
<223> Asp or Asn

<400> 14  
Thr Xaa Glu Xaa Xaa Xaa Xaa Xaa Ser Pro Xaa Xaa Xaa  
1 5 10

<210> 15  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<220>  
<221> MOD\_RES  
<222> (1)  
<223> hydrophobic amino acid

<220>  
<221> MOD\_RES  
<222> (4)  
<223> Ala or Gly

<220>  
<221> MOD\_RES  
<222> (6)..(7)  
<223> variable amino acid

<400> 15  
Xaa Glu Pro Xaa Ser Xaa Xaa Lys

1 5

<210> 16  
<211> 7  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
peptide

<220>  
<221> MOD\_RES  
<222> (1)  
<223> hydrophobic amino acid

<220>  
<221> MOD\_RES  
<222> (2)..(3)  
<223> variable amino acid

<220>  
<221> MOD\_RES  
<222> (5)  
<223> variable amino acid

<220>  
<221> MOD\_RES  
<222> (7)  
<223> hydrophobic amino acid

<400> 16  
Xaa Xaa Xaa Ser Xaa Asn Xaa  
1 5

<210> 17  
<211> 7  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
peptide

<400> 17  
Ala Lys Arg Gly Thr Ile Tyr  
1 5

<210> 18  
<211> 750  
<212> PRT  
<213> Streptococcus pneumoniae

<400> 18

Met	Lys	Trp	Thr	Lys	Arg	Val	Ile	Arg	Tyr	Ala	Thr	Lys	Asn	Arg	Lys	1	5	10	15
Ser	Pro	Ala	Glu	Asn	Arg	Arg	Arg	Val	Gly	Lys	Ser	Leu	Ser	Leu	Leu	20	25	30	
Ser	Val	Phe	Val	Phe	Ala	Ile	Phe	Leu	Val	Asn	Phe	Ala	Val	Ile	Ile	35	40	45	
Gly	Thr	Gly	Thr	Arg	Phe	Gly	Thr	Asp	Leu	Ala	Lys	Glu	Ala	Lys	Lys	50	55	60	
Val	His	Gln	Thr	Thr	Arg	Thr	Val	Pro	Ala	Lys	Arg	Gly	Thr	Ile	Tyr	65	70	75	80
Asp	Arg	Asn	Gly	Val	Pro	Ile	Ala	Glu	Asp	Ala	Thr	Ser	Tyr	Asn	Val	85	90	95	
Tyr	Ala	Val	Ile	Asp	Glu	Asn	Tyr	Lys	Ser	Ala	Thr	Gly	Lys	Ile	Leu	100	105	110	
Tyr	Val	Glu	Lys	Thr	Gln	Phe	Asn	Lys	Val	Ala	Glu	Val	Phe	His	Lys	115	120	125	
Tyr	Leu	Asp	Met	Glu	Glu	Ser	Tyr	Val	Arg	Glu	Gln	Leu	Ser	Gln	Pro	130	135	140	
Asn	Leu	Lys	Gln	Val	Ser	Phe	Gly	Ala	Lys	Gly	Asn	Gly	Ile	Thr	Tyr	145	150	155	160
Ala	Asn	Met	Met	Ser	Ile	Lys	Lys	Glu	Leu	Glu	Ala	Ala	Glu	Val	Lys	165	170	175	
Gly	Ile	Asp	Phe	Thr	Thr	Ser	Pro	Asn	Arg	Ser	Tyr	Pro	Asn	Gly	Gln	180	185	190	
Phe	Ala	Ser	Ser	Phe	Ile	Gly	Leu	Ala	Gln	Leu	His	Glu	Asn	Glu	Asp	195	200	205	
Gly	Ser	Lys	Ser	Leu	Leu	Gly	Thr	Ser	Gly	Met	Glu	Ser	Ser	Leu	Asn	210	215	220	
Ser	Ile	Leu	Ala	Gly	Thr	Asp	Gly	Ile	Ile	Thr	Tyr	Glu	Lys	Asp	Arg	225	230	235	240
Leu	Gly	Asn	Ile	Val	Pro	Gly	Thr	Glu	Gln	Val	Ser	Gln	Arg	Thr	Met	245	250	255	
Asp	Gly	Lys	Asp	Val	Tyr	Thr	Thr	Ile	Ser	Ser	Pro	Leu	Gln	Ser	Phe	260	265	270	
Met	Glu	Thr	Gln	Met	Asp	Ala	Phe	Gln	Glu	Lys	Val	Lys	Gly	Lys	Tyr	275	280	285	
Met	Thr	Ala	Thr	Leu	Val	Ser	Ala	Lys	Thr	Gly	Glu	Ile	Leu	Ala	Thr	290	295	300	

Thr	Gln	Arg	Pro	Thr	Phe	Asp	Ala	Asp	Thr	Lys	Glu	Gly	Ile	Thr	Glu	305	310	315	320
Asp	Phe	Val	Trp	Arg	Asp	Ile	Leu	Tyr	Gln	Ser	Asn	Tyr	Glu	Pro	Gly	325	330	335	
Ser	Thr	Met	Lys	Val	Met	Met	Leu	Ala	Ala	Ala	Ile	Asp	Asn	Asn	Thr	340	345	350	
Phe	Pro	Gly	Gly	Glu	Val	Phe	Asn	Ser	Ser	Glu	Leu	Lys	Ile	Ala	Asp	355	360	365	
Ala	Thr	Ile	Arg	Asp	Trp	Asp	Val	Asn	Glu	Gly	Leu	Thr	Gly	Gly	Arg	370	375	380	
Met	Met	Thr	Phe	Ser	Gln	Gly	Phe	Ala	His	Ser	Ser	Asn	Val	Gly	Met	385	390	395	400
Thr	Leu	Leu	Glu	Gln	Lys	Met	Gly	Asp	Ala	Thr	Trp	Leu	Asp	Tyr	Leu	405	410	415	
Asn	Arg	Phe	Lys	Phe	Gly	Val	Pro	Thr	Arg	Phe	Gly	Leu	Thr	Asp	Glu	420	425	430	
Tyr	Ala	Gly	Gln	Leu	Pro	Ala	Asp	Asn	Ile	Val	Asn	Ile	Ala	Gln	Ser	435	440	445	
Ser	Phe	Gly	Gln	Gly	Ile	Ser	Val	Thr	Gln	Thr	Gln	Met	Ile	Arg	Ala	450	455	460	
Phe	Thr	Ala	Ile	Ala	Asn	Asp	Gly	Val	Met	Leu	Glu	Pro	Lys	Phe	Ile	465	470	475	480
Ser	Ala	Ile	Tyr	Asp	Pro	Asn	Asp	Gln	Thr	Ala	Arg	Lys	Ser	Gln	Lys	485	490	495	
Glu	Ile	Val	Gly	Asn	Pro	Val	Ser	Lys	Asp	Ala	Ala	Ser	Leu	Thr	Arg	500	505	510	
Thr	Asn	Met	Val	Leu	Val	Gly	Thr	Asp	Pro	Val	Tyr	Gly	Thr	Met	Tyr	515	520	525	
Asn	His	Ser	Thr	Gly	Lys	Pro	Thr	Val	Thr	Val	Pro	Gly	Gln	Asn	Val	530	535	540	
Ala	Leu	Lys	Ser	Gly	Thr	Ala	Gln	Ile	Ala	Asp	Glu	Lys	Asn	Gly	Gly	545	550	555	560
Tyr	Leu	Val	Gly	Leu	Thr	Asp	Tyr	Ile	Phe	Ser	Ala	Val	Ser	Met	Ser	565	570	575	
Pro	Ala	Glu	Asn	Pro	Asp	Phe	Ile	Leu	Tyr	Val	Thr	Val	Gln	Gln	Pro	580	585	590	
Glu	His	Tyr	Ser	Gly	Ile	Gln	Leu	Gly	Glu	Phe	Ala	Asn	Pro	Ile	Leu	595	600	605	

Glu	Arg	Ala	Ser	Ala	Met	Lys	Asp	Ser	Leu	Asn	Leu	Gln	Thr	Thr	Ala
610						615					620				
Lys	Ala	Leu	Glu	Gln	Val	Ser	Gln	Gln	Ser	Pro	Tyr	Pro	Met	Pro	Ser
625					630					635					640
Val	Lys	Asp	Ile	Ser	Pro	Gly	Asp	Leu	Ala	Glu	Glu	Leu	Arg	Arg	Asn
			645						650					655	
Leu	Val	Gln	Pro	Ile	Val	Val	Gly	Thr	Gly	Thr	Lys	Ile	Lys	Asn	Ser
		660						665					670		
Ser	Ala	Glu	Glu	Gly	Lys	Asn	Leu	Ala	Pro	Asn	Gln	Gln	Val	Leu	Ile
	675						680					685			
Leu	Ser	Asp	Lys	Ala	Glu	Glu	Val	Pro	Asp	Met	Tyr	Gly	Trp	Thr	Lys
	690					695					700				
Glu	Thr	Ala	Glu	Thr	Leu	Ala	Lys	Trp	Leu	Asn	Ile	Glu	Leu	Glu	Phe
705					710					715					720
Gln	Gly	Ser	Gly	Ser	Thr	Val	Gln	Lys	Gln	Asp	Val	Arg	Ala	Asn	Thr
			725						730					735	
Ala	Ile	Lys	Asp	Ile	Lys	Lys	Ile	Thr	Leu	Thr	Leu	Gly	Asp		
		740						745					750		